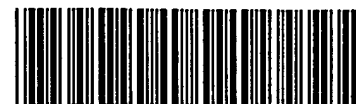


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The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/564,617
Source: TFWP
Date Processed by STIC: 1-30-06

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DATE: 01/30/2006

PATENT APPLICATION: US/10/564,617

TIME: 14:44:31

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Output Set : N:\CRF4\01302006\J564617.raw

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3 <110> APPLICANT: Kwang , Jimmy
4     Ling, Ai Ee
5     Ooi, Eng Eong
6     Chng, Hiok Hee
8 <120> TITLE OF INVENTION: Diagnostics for SARS Virus
10 <130> FILE REFERENCE: 2577-162
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/564,617
C--> 12 <141> CURRENT FILING DATE: 2006-01-13
12 <150> PRIOR APPLICATION NUMBER: 60/486,918
13 <151> PRIOR FILING DATE: 2003-07-15
15 <150> PRIOR APPLICATION NUMBER: PCT/US04/003307
16 <151> PRIOR FILING DATE: 2004-02-04
18 <160> NUMBER OF SEQ ID NOS: 25
20 <170> SOFTWARE: PatentIn version 3.2
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24 <212> TYPE: DNA
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38 Thr Phe Gly Gly Pro Thr Asp Ser Thr Asp Asn Asn Gln Asn Gly Gly
39          20          25          30
41 cgc aat ggg gca agg cca aaa cag cgc cga ccc caa ggt tta ccc aat      144
42 Arg Asn Gly Ala Arg Pro Lys Gln Arg Arg Pro Gln Gly Leu Pro Asn
43          35          40          45
45 aat act gcg tct tgg ttc aca gct ctc act cag cat ggc aag gag gaa      192
46 Asn Thr Ala Ser Trp Phe Thr Ala Leu Thr Gln His Gly Lys Glu Glu
47          50          55          60
49 ctt aga ttc cct cga ggc cag ggc gtt cca atc aac acc aat agt ggt      240
50 Leu Arg Phe Pro Arg Gly Gln Gly Val Pro Ile Asn Thr Asn Ser Gly
51 65          70          75          80
53 cca gat gac caa att ggc tac tac cga aga gct acc cga cga gtt cgt      288
54 Pro Asp Asp Gln Ile Gly Tyr Tyr Arg Arg Ala Thr Arg Arg Val Arg
55          85          90          95
57 ggt ggt gac ggc aaa atg aaa gag ctc agc ccc aga tgg tac ttc tat      336
58 Gly Gly Asp Gly Lys Met Lys Glu Leu Ser Pro Arg Trp Tyr Phe Tyr
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62	Tyr	Leu	Gly	Thr	Gly	Pro	Glu	Ala	Ser	Leu	Pro	Tyr	Gly	Ala	Asn	Lys	
63			115					120					125				
65	gaa	ggc	atc	gta	tgg	gtt	gca	act	gag	gga	gcc	ttg	aac	aca	ccc	aaa	432
66	Glu	Gly	Ile	Val	Trp	Val	Ala	Thr	Glu	Gly	Ala	Leu	Asn	Thr	Pro	Lys	
67		130					135					140					
69	gac	cac	att	ggc	acc	cgc	aat	cct	aat	aac	aat	gct	gcc	acc	gtg	cta	480
70	Asp	His	Ile	Gly	Thr	Arg	Asn	Pro	Asn	Asn	Asn	Ala	Ala	Thr	Val	Leu	
71	145					150					155					160	
73	caa	ctt	cct	caa	gga	aca	aca	ttg	cca	aaa	ggc	ttc	tac	gca	gag	gga	528
74	Gln	Leu	Pro	Gln	Gly	Thr	Thr	Leu	Pro	Lys	Gly	Phe	Tyr	Ala	Glu	Gly	
75				165						170					175		
77	agc	aga	ggc	ggc	agt	caa	gcc	tct	tct	cgc	tcc	tca	tca	cgt	agt	cgc	576
78	Ser	Arg	Gly	Gly	Ser	Gln	Ala	Ser	Ser	Arg	Ser	Ser	Ser	Arg	Ser	Arg	
79			180						185					190			
81	ggt	aat	tca	aga	aat	tca	act	cct	ggc	agc	agt	agg	gga	aat	tct	cct	624
82	Gly	Asn	Ser	Arg	Asn	Ser	Thr	Pro	Gly	Ser	Ser	Arg	Gly	Asn	Ser	Pro	
83		195						200					205				
85	gct	cga	atg	gct	agc	gga	ggt	ggt	gaa	act	gcc	ctc	gcg	cta	ttg	ctg	672
86	Ala	Arg	Met	Ala	Ser	Gly	Gly	Gly	Glu	Thr	Ala	Leu	Ala	Leu	Leu	Leu	
87		210					215						220				
89	cta	gac	aga	ttg	aac	cag	ctt	gag	agc	aaa	gtt	tct	ggt	aaa	ggc	caa	720
90	Leu	Asp	Arg	Leu	Asn	Gln	Leu	Glu	Ser	Lys	Val	Ser	Gly	Lys	Gly	Gln	
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93	caa	caa	caa	ggc	caa	act	gtc	act	aag	aaa	tct	gct	gct	gag	gca	tct	768
94	Gln	Gln	Gln	Gly	Gln	Thr	Val	Thr	Lys	Lys	Ser	Ala	Ala	Glu	Ala	Ser	
95				245						250				255			
97	aaa	aag	cct	cgc	caa	aaa	cgt	act	gcc	aca	aaa	cag	tac	aac	gtc	act	816
98	Lys	Lys	Pro	Arg	Gln	Lys	Arg	Thr	Ala	Thr	Lys	Gln	Tyr	Asn	Val	Thr	
99			260						265					270			
101	caa	gca	ttt	ggg	aga	cgt	ggt	cca	gaa	caa	acc	caa	gga	aat	ttc	ggg	864
102	Gln	Ala	Phe	Gly	Arg	Arg	Gly	Pro	Glu	Gln	Thr	Gln	Gly	Asn	Phe	Gly	
103			275					280						285			
105	gac	caa	gac	cta	atc	aga	caa	gga	act	gat	tac	aaa	cat	tgg	ccg	caa	912
106	Asp	Gln	Asp	Leu	Ile	Arg	Gln	Gly	Thr	Asp	Tyr	Lys	His	Trp	Pro	Gln	
107		290					295					300					
109	att	gca	caa	ttt	gct	cca	agt	gcc	tct	gca	ttc	ttt	gga	atg	tca	cgc	960
110	Ile	Ala	Gln	Phe	Ala	Pro	Ser	Ala	Ser	Ala	Phe	Phe	Gly	Met	Ser	Arg	
111	305					310					315					320	
113	att	ggc	atg	gaa	gtc	aca	cct	tcg	gga	aca	tgg	ctg	act	tat	cat	gga	1008
114	Ile	Gly	Met	Glu	Val	Thr	Pro	Ser	Gly	Thr	Trp	Leu	Thr	Tyr	His	Gly	
115				325						330				335			
117	gcc	att	aaa	ttg	gat	gac	aaa	gat	cca	caa	ttc	aaa	gac	aac	gtc	ata	1056
118	Ala	Ile	Lys	Leu	Asp	Asp	Lys	Asp	Pro	Gln	Phe	Lys	Asp	Asn	Val	Ile	
119			340						345				350				
121	ctg	ctg	aac	aag	cac	att	gac	gca	tac	aaa	aca	ttc	cca	cca	aca	gag	1104
122	Leu	Leu	Asn	Lys	His	Ile	Asp	Ala	Tyr	Lys	Thr	Phe	Pro	Pro	Thr	Glu	
123			355					360					365				
125	cct	aaa	aag	gac	aaa	aag	aaa	aag	act	gat	gaa	gct	cag	cct	ttg	ccg	1152

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129 cag aga caa aag aag cag ccc act gtg act ctt ctt cct gcg gct gac      1200
130 Gln Arg Gln Lys Lys Gln Pro Thr Val Thr Leu Pro Ala Ala Asp
131 385      390      395      400
133 atg gat gat ttc tcc aga caa ctt caa aat tcc atg agt gga gct tct      1248
134 Met Asp Asp Phe Ser Arg Gln Leu Gln Asn Ser Met Ser Gly Ala Ser
135      405      410      415
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143 <211> LENGTH: 422
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154      20      25      30
157 Arg Asn Gly Ala Arg Pro Lys Gln Arg Arg Pro Gln Gly Leu Pro Asn
158      35      40      45
161 Asn Thr Ala Ser Trp Phe Thr Ala Leu Thr Gln His Gly Lys Glu Glu
162      50      55      60
165 Leu Arg Phe Pro Arg Gly Gln Gly Val Pro Ile Asn Thr Asn Ser Gly
166 65      70      75      80
169 Pro Asp Asp Gln Ile Gly Tyr Tyr Arg Arg Ala Thr Arg Arg Val Arg
170      85      90      95
173 Gly Gly Asp Gly Lys Met Lys Glu Leu Ser Pro Arg Trp Tyr Phe Tyr
174      100      105      110
177 Tyr Leu Gly Thr Gly Pro Glu Ala Ser Leu Pro Tyr Gly Ala Asn Lys
178      115      120      125
181 Glu Gly Ile Val Trp Val Ala Thr Glu Gly Ala Leu Asn Thr Pro Lys
182      130      135      140
185 Asp His Ile Gly Thr Arg Asn Pro Asn Asn Asn Ala Ala Thr Val Leu
186 145      150      155      160
189 Gln Leu Pro Gln Gly Thr Thr Leu Pro Lys Gly Phe Tyr Ala Glu Gly
190      165      170      175
193 Ser Arg Gly Gly Ser Gln Ala Ser Ser Arg Ser Ser Ser Arg Ser Arg
194      180      185      190
197 Gly Asn Ser Arg Asn Ser Thr Pro Gly Ser Ser Arg Gly Asn Ser Pro
198      195      200      205
201 Ala Arg Met Ala Ser Gly Gly Gly Glu Thr Ala Leu Ala Leu Leu Leu
202      210      215      220
205 Leu Asp Arg Leu Asn Gln Leu Glu Ser Lys Val Ser Gly Lys Gly Gln
206 225      230      235      240
209 Gln Gln Gln Gly Gln Thr Val Thr Lys Lys Ser Ala Ala Glu Ala Ser
210      245      250      255
213 Lys Lys Pro Arg Gln Lys Arg Thr Ala Thr Lys Gln Tyr Asn Val Thr

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217 Gln Ala Phe Gly Arg Arg Gly Pro Glu Gln Thr Gln Gly Asn Phe Gly
218          275          280          285
221 Asp Gln Asp Leu Ile Arg Gln Gly Thr Asp Tyr Lys His Trp Pro Gln
222          290          295          300
225 Ile Ala Gln Phe Ala Pro Ser Ala Ser Ala Phe Phe Gly Met Ser Arg
226 305          310          315          320
229 Ile Gly Met Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr His Gly
230          325          330          335
233 Ala Ile Lys Leu Asp Asp Lys Asp Pro Gln Phe Lys Asp Asn Val Ile
234          340          345          350
237 Leu Leu Asn Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro Thr Glu
238          355          360          365
241 Pro Lys Lys Asp Lys Lys Lys Lys Thr Asp Glu Ala Gln Pro Leu Pro
242          370          375          380
245 Gln Arg Gln Lys Lys Gln Pro Thr Val Thr Leu Leu Pro Ala Ala Asp
246 385          390          395          400
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257 <210> SEQ ID NO: 3
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259 <212> TYPE: DNA
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270 1          5          10          15
272 gac cgg tgc acc act ttt gat gat gtt caa gct cct aat tac act caa      96
273 Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
274          20          25          30
276 cat act tca tct atg agg ggg gtt tac tat cct gat gaa att ttt aga     144
277 His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
278          35          40          45
280 tca gac act ctt tat tta act cag gat tta ttt ctt cca ttt tat tct     192
281 Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
282          50          55          60
284 aat gtt aca ggg ttt cat act att aat cat acg ttt ggc aac cct gtc     240
285 Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
286 65          70          75          80
288 ata cct ttt aag gat ggt att tat ttt gct gcc aca gag aaa tca aat     288
289 Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
290          85          90          95
292 gtt gtc cgt ggt tgg gtt ttt ggt tct acc atg aac aac aag tca cag     336
293 Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln

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294		100		105		110		
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298								
300	aac	ttt	gaa	ttg	tgt	gac	aac	cct
301	Asn	Phe	Glu	Leu	Cys	Asp	Asn	Pro
302								
304	ggt	aca	cag	aca	cat	act	atg	ata
305	Gly	Thr	Gln	Thr	His	Thr	Met	Ile
306	145							
308	ttc	gag	tac	ata	tct	gat	gcc	ttt
309	Phe	Glu	Tyr	Ile	Ser	Asp	Ala	Phe
310								
312	ggt	aat	ttt	aaa	cac	tta	cga	gag
313	Gly	Asn	Phe	Lys	His	Leu	Arg	Glu
314								
316	ttt	ctc	tat	ggt	tat	aag	ggc	tat
317	Phe	Leu	Tyr	Val	Tyr	Lys	Gly	Tyr
318								
320	cta	cct	tct	ggt	ttt	aac	act	ttg
321	Leu	Pro	Ser	Gly	Phe	Asn	Thr	Leu
322								
324	ggt	att	aac	att	aca	aat	ttt	aga
325	Gly	Ile	Asn	Ile	Thr	Asn	Phe	Arg
326	225							
328	gct	caa	gac	att	tgg	ggc	acg	tca
329	Ala	Gln	Asp	Ile	Trp	Gly	Thr	Ser
330								
332	tta	aag	cca	act	aca	ttt	atg	ctc
333	Leu	Lys	Pro	Thr	Thr	Phe	Met	Leu
334								
336	aca	gat	gct	ggt	gat	tgt	tct	caa
337	Thr	Asp	Ala	Val	Asp	Cys	Ser	Gln
338								
340	tct	ggt	aag	agc	ttt	gag	att	gac
341	Ser	Val	Lys	Ser	Phe	Glu	Ile	Asp
342								
344	ttc	agg	ggt	ggt	ccc	tca	gga	gat
345	Phe	Arg	Val	Val	Pro	Ser	Gly	Asp
346	305							
348	aac	ttg	tgt	cct	ttt	gga	gag	ggt
349	Asn	Leu	Cys	Pro	Phe	Gly	Glu	Val
350								
352	gtc	tat	gca	tgg	gag	aga	aaa	aaa
353	Val	Tyr	Ala	Trp	Glu	Arg	Lys	Lys
354								
356	tct	gtg	ctc	tac	aac	tca	aca	ttt
357	Ser	Val	Leu	Tyr	Asn	Ser	Thr	Phe
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/564,617

DATE: 01/30/2006

TIME: 14:44:32

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date